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alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of the respective reference strain, IM2169 or IM2394, as shown in ID SEQ No. 1 or 3, by total or partial deletion of at least one domain of said IM2169 or IM2394 type Tbp2 subunit, provided the first and second domains are not totally deleted simultaneously.--

Claim 55, line 2, please delete "derived" and substitute therefor --obtained--.

Claim 56, line 2, please delete "derived" and substitute therefor --obtained--.

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--57. (Once amended) A polypeptide according to claim 55, having an amino acid sequence which is [derived] obtained from the sequence of the IM2394 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2394, by total deletion of the third domain and by partial or total deletion of the second domain of said IM2394 type Tbp2 subunit.--

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--58. (Once amended) A polypeptide according to claim 57, having an amino acid sequence which is [derived] obtained from the sequence of the IM2394 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence

of the Tbp2 subunit of reference strain IM2394, by total deletion of the third domain, by partial or total deletion of the second domain of said IM2394 type Tbp2 subunit and which contains in full the first domain of the sequence from which it is derived.--

--59. (Once amended) A polypeptide according to claim 57, having an amino acid sequence which is further [derived] obtained from the sequence of the IM2394 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2394, by partial deletion of the first domain of said IM2394 type Tbp2 subunit.--

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--60. (Once amended) A polypeptide according to claim 58, having an amino acid sequence which is [derived] obtained from the sequence of the IM2394 type of Tbp2 subunit whose first, second and third domain are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2394, by deletion of the region of the second domain of the IM2394 Tbp2 subunit which is homologous to the region of the second domain of the IM2394 Tbp2 subunit, extending [form] from the amino acid in any one of positions 326 to 341 to amino acid in position 442.--

--61. (Once amended) A polypeptide according to claim 55, having an amino acid sequence which is [derived] obtained from the

sequence of the IM2394 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequences of the Tbp2 subunit of reference strain IM2394, by partial deletion of the first domain of said IM2394 type Tbp2 subunit.--

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--62. (Once amended) A polypeptide according to claim 61, having an amino acid sequence which is [derived] obtained from the sequence of the IM2394 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2394, by deletion of all or part of the region which is homologous to the region of the first domain of said IM2394 type Tbp2 subunit, extending from amino acid in position 1 to amino acid in position 266.--

Claim 63, line 2, please delete "derived" and substitute therefor --obtained--.

Claim 64, line 2, please delete "derived" and substitute therefor --obtained--.

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--65. (Once amended) A polypeptide according to claim 63, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence

of the Tbp2 subunit of reference strain IM2169 by partial deletion of the second domain of said IM2169 type Tbp2 subunit.--

--66. (Once amended) A polypeptide according to claim 65, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid ~~identity~~ alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the IM2169 Tbp2 subunit; by deletion of at least one of the regions of the second domain of the said IM2169 type Tbp2 subunit which are homologous to regions of IM2169 Tbp2 subunit, extending:

- D4*
CSM
- (i) from amino acid in position 362 to amino acid in position 379;
 - (ii) from amino acid in position 418 to amino acid in position 444;
 - (iii) from amino acid in position 465 to amino acid in position 481;
 - (iv) from amino acid in position 500 to amino acid in position 520.--

--67. (Once amended) A polypeptide according to claim 66, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit, whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid ~~identity~~ alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the IM2169 Tbp2 subunit, by deletion of the regions of the second domain of said IM2169 type Tbp2 subunit which are homologous to said regions (i) to (iv) of the IM2169 Tbp2 subunit.--

--68. (Once amended) A polypeptide according to claim 66 or 67, having an amino acid sequence which is [derived] obtained from

the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2169 by partial deletion of the second domain of said IM2169 type Tbp2 subunit and which contains in full, the first and third domains of said IM2169 type Tbp2 subunit.--

--69. (Once amended) A polypeptide according to claim 66 or 67, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2169 by partial deletion of the second domain, by partial or total deletion of the first domain and/or by partial or total deletion of the third domain of said IM2169 type Tbp2 subunit.--

--70. (Once amended) A polypeptide according to claim 63, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2169, by total deletion

of the third domain and by partial or total deletion of the second domain of said IM2169 type Tbp2 subunit.--

--71. (Once amended) A polypeptide to claim 70, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequences for the Tbp2 subunit of reference strain IM2169, by total deletion of the third domain, by partial or total deletion of the second domain of said IM2169 type Tbp2 subunit and which contains in full the first domain of the sequence from which it is [derived] obtained.--

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--72. (Once amended) A polypeptide according to claim 70, having an amino acid sequence which is further [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequences of the Tbp2 subunit of reference strain IM2169, by partial deletion of the first domain of said IM2169 type Tbp2 subunit.--

--73. (Once amended) A polypeptide according to claim 71, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions

while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2169, by deletion of the region of the second domain of the said IM2169 type Tbp2 subunit which is homologous to the region of the second domain of the IM2169 Tbp2 subunit, extending from the amino acid in any one of positions 346 to 361 to amino acid in position 543.--

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--74. (Once amended) A polypeptide according to claim 70, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2169, by partial deletion of the first domain of said IM2394 type Tbp2 subunit.--

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--75. (Once amended) A polypeptide according to claim 74, having an amino acid sequence which is [derived] obtained from the sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2169, by deletion of all or part of the region which is homologous to the region of the first domain of said IM2169 type Tbp2 subunit, extending from amino acid in position 1 to amino acid in position 281.--

--76. (Once amended) A polypeptide according to claim 63, having an amino acid sequence which is [derived] obtained from the

sequence of the IM2169 type Tbp2 subunit whose first, second and third domains are defined by [maximal homology alignment] maximum amino acid identity alignment versus the total number of positions while introducing vacant positions artificially with the sequence of the Tbp2 subunit of reference strain IM2169, by partial or total deletion of the first domain and/or by partial or total deletion of the third domain of said IM2169 type Tbp2 subunit and which contains in full, the second domain of said IM2169 type Tbp2 subunit.--

REMARKS

By this amendment, Applicants have amended the claims so as to delete language considered objectionable by the Examiner and overcome the outstanding rejections under 35 U.S.C. § 112 and 35 U.S.C. § 102(b). In addition, reference to sequence identifiers as required by the Examiner are now provided. For the reasons as stated below, Applicants submit that upon entrance of the present amendment, the outstanding rejections will be overcome and the case will be suitable for allowance.

In the claims in their present form, the term "derived" which had been objected to by the Examiner, has now been replaced by the word "obtained", and Applicants submit that this term would be readily understood by one skilled in this art and would enable such a person to make and use the invention. In addition, Applicants now have replaced the term "maximal homology alignment" which was objected to by the Examiner with the phrase "maximum amino acid